

source

```

L. .849
/organism="Tetraodon n

```

```

/db_xref="taxon:99883"
/clone_1b="G"
/clone_1b="G"
/note="Genoscope sequence ID : COAG166BH11LP1-end : T7
BASE COUNT      169 a      219 c      221 g      216 t      24 others
ORIGIN

```

Query Match	53.7%	Score 88;	DB 17;	Length 849;
Best Local Similarity	74.6%;	Pred. No. 6e-16;		
Matches 103; Conservative	5;	Mismatches 30;	Indels 0;	Gaps 0

```

2/ TTTTGTACTTGAGAGATAGACATGAGACATCTCCATAAACTTTGAAGATTACG 86
||||| ||||||| ||| ||| ||||||| ||| : ||||||| |||
Db 179 TTTTGTACTTGAAGATCGAGATGAGACATCGGAGGAGACMMTTGAAGATCACC 23

```

QY 87 ATTTTGGGTGGCGAGGGAATGCGACACGACCAAAATGAGCAGACGACCTATG 146
||||| ||| ||| ||| ||| ||| : ||| ||| | : ||| ||| |||
Db 239 ATTTGGGGCTGGCGAGGAGATGCGACAAAMMACCAAGATGTGGCTGMAAGCACCTACT 298

QY	14	CCTGGATGGCCCCAGAG	164
Db	299	CCTGGATGGCCCCCTGAG	316

RESULT 6	
AM658260	
LOCUS	486 bp
DEFINITION	mRNA
94142 MARC IBOV Bos taurus cDNA 5'	linear
ACCSSION	aa658260
	mRNA sequence.
	EST 25-APR-2001

VERSION	AW658260.1	GI:7424086
KEYWORDS	EST.	
SOURCE	COW.	

ORGANISM	REFERENCE
<i>Bos taurus</i>	Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T., et al. 1996
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bovinae; Bos.	1 (bases 1 to 486)

TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL	Genome Res. 11 (4), 626-630 (2001)
MEDLINE	21180013
COMMENT	Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with `mpileup`
v0.8809094.e. Vector identified by `cross-match` with the `-mscore 18`
and `-mismatch 12` options.

FEATURES

FORWARD:	AGGAACAGCTATGACCA
BACKWARD:	GTTTCCCAGTCACGAG
Plate:	60
row:	N
column:	23
Seq primer:	ATTAGGTGACACTTAG
Location/Qualifiers	

Source

```
/organism="Bos taurus"  
/db_xref="taxon:9913"  
/clone_lib="MARC 1BOV"  
/tissue_type="pooled"  
/ab_bect="T0100"
```

BASE COUNT	89 a	155 c	140 g	101 t	1 others
ORIGIN					

Query Match	51.6%;	Score 84.6;	DB 10;	Length 486;
Best Local Similarity	69.9%;	Pred. No. 5.3e-15;		
Matches 114; Conservative	0;	Mismatches 49;	Indels 0;	Gaps 0

QY 2 CACCGGACATCAAGCGCAGGAAATATTTTGTCTACTTGTAGAAAGATAGAACATGATGACATC 61

Dy 62 TGCATTAACCTTTGAGATTACAGATTTGGCTTGGCGAGGAATGGCACGACC ACC 121
| | | | |
Db 180 GAGCACAAGACCCGTAGATCAACGACTTCGGTCTGGCCCCGTGATGGCACAAAAC CAG 239

QY 122 AAATGAGCACAGCAGGCACCTATGCTGGATGGCCCCAAGA 164
||||| | | ||||| ||||| ||||| |||||
D0 240 CAAATGAGTGTCTGGCGGCCACTATGCTGGATGGCTTCCTGAGG 282

RESULT 7			
BE682782			
LOCUS	BE682782	551 bp	
DEFINITION	111081. MARC 4BOV Bos taurus CDNA 5', mRNA	linear	EST 25-APR-2001
ACCESSION	BE682782		

ORGANISM

REFERENCE AUTHORS

TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL	Genome Res. 11 (4), 626-630 (2001)
MEDLINE	21180013
COMMENT	Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -minmatch 12 options.
PCR Primers

FORWARD: AGGAACACGCTATGACCAT
 BACKWARD: GTTTCCTCAGTCACGACG
 Plate: 76 row: M column: 8
 Seq primer: ATTTCGTGACACTATAG

FEATURES

source

```

/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 4BOY"
/tissue_type="pooled"
/lab_host="DH10B"
/notice="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI
Library made from pooled tissue from day 20 and day 40
embryos."

```

Query Match	51.6%;	Score 84.6;	DB 10;	Length 551;
Best Local Similarity	69.9%;	Pred. No. 5.5e-15;		
Matches 114; Conservative	0;	Mismatches 49;	Indels 0;	Gaps 0;

QY 2 CACCGGACATCAAGGCAGGAATAATTTCCTACTTGGAAGATAGMACATGATGATC 61
||||| ||| ||||| | ||||| ||| ||| ||| ||| ||| |||
Db 309 CACCGAGACCTCAAGTCCACAACAACTTCTGCTGCTGAGCCCATTTGAAGGTGACGACATG 368

OY	62	TGCATTAACCTTTGAGATTACAGATTGGTGGTGCGAGGAAATGGCACAGACCACC	121
Dd	369	GAGCACAAGACCCCTGGAAGATACGCACTTCGGTCTGGGCCCTGTAGTGGACAAAACACG	428
OY	122	AAAAAGACACAGCAGGACCATTCATGCTGATGGCCCCAGAAG	164
Dd	429	CAATGATGCTGGGGGACACTTATGCGATGGCTCTCTAGG	471
RESULT 8			
B0604135/c		791 bp	mRNA linear EST 24-JUN-2002
LOCUS			
DEFINITION			
ACCESSION	B0604135		
VERSION	M1-P-CPI-nzb-a-19-0-UI-s1		
KEYWORDS	M1-P-CPI-nzb-a-19-0-UI 3'		
SOURCE	EST.		
ORGANISM	B0604135.1 GI:21550861		
REFERENCE			
AUTHORS	Sus scrofa		
TITLE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.		
JOURNAL MEDLINE COMMENT	1 (bases 1 to 791) Bonaldio,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene discovery Genome Res. 6 (9), 791-806 (1996)		
FEATURES			
SOURCE	Contact: Tuggle CK Molecular Genetics Laboratory, Department of Animal Science Iowa State University 201 Kildee Hall, Ames, IA 50011-3150, USA Tel: 5152944252 Fax: 5152942401 Email: cktuggle@iastate.edu Tissue Procurement: Dr. Chris Tuggle, Iowa State University cDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com). Seq primer: M13 FORWARD POLYA-No.		
FEATURES			
SOURCE	location/Qualifiers 1..791 /organism="Sus scrofa" /strain="crossbreed" /db_xref="taxon:9823" /clone="M1-P-CPI-nzb-a-19-0-UI" /clone_1id="M1-P-CPI" /lab_host="DH10B (Life Technologies)" /note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I, Site_2: EcoRI. The M1-P-CPI library is normalized library derived from uterus tissue. For a detailed description of the library from which this clone was derived, please visit our web site at http://piglet.genome.iastate.edu/. The procedure used to create this library has been previously described (Bonaldio , Lennon and Soares, Genome Research 6: 791-806, 1996) TAG-Seq=None found"		
BASE COUNT	143 a 251 c 246 g 151 t		
ORIGIN			
Query Match	51.6%	Score 84.6:	DB 14;
Best Local Similarity	69.9%	Pred. No. 6.2e-15;	
Matches 114:	Conservative 0;	Mismatches 49;	Indels 0;
Gaps 0;			
OY	2	CACCGGACATCAACGCGAATAATTTTGGTACTAGAGATGAGCATGATGATC	61
Dd	694	CACGAGACCTCAATTCACACACACTTCTGCTGTCGACGCCATTCGAAAGTACACATG	635
OY	62	TGCATTAACCTTTGAGATTACAGATTGGTGGTGCGAGGAAATGGCACAGACACC	121

QY	LOCUS	DEFINITION	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	BASE COUNT	ORIGIN
634	GAGCAACAAGACCC	CGTAGATCATCTGACTTGGCCCTGGGCGCGGAGTGGACACAAAACACG	575							
122	AAATGAGCAGACGACGAC	CCTATGCTGATGGCCCCAGAG	164							
574	CAATGAGTGTCTGGCGG	CACCTATGCTGATGGCTCTCTGAGG	532							
RESULT 9	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			
AU125482	AU125482	NT2RM4 Homo sapiens cDNA clone NT2RM4001663 5', mRNA	746 bp	mRNA	linear	EST 01-AUG-2002				
		sequence.	AU125482							
		EST.	AU125482.1	GI:10950198						
		human.								
		Homo sapiens								
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
		1 (bases 1 to 746)								
		Ota,T., Wakamatsu,A., Ozawa,M., Ishi,S., Saito,K., Yamamoto,J.,								
		Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and								
		Isogai,T.								
		HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishi,S.,								
		Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki								
		,Y., Sugano,S., Isogai,T.)								
		Unpublished (2000)								
		Contact: Takao Isogai								
		Genomics Laboratory								
		Helix Research Institute								
		1532-3 Yana, Kisarazu, Chiba 292-0812, Japan								
		Tel: 81-438-52-3975								
		Fax: 81-438-52-3986								
		Email: genomics@hri.co.jp								
		HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix								
		Research Institute; cDNA library construction; Department of								
		Virology, Institute of Medical Science, University of Tokyo, and								
		Helix Research Institute.								
		Location/Qualifiers								
		1..746								
		/organism="Homo sapiens"								
		/db_xref="taxon:9606"								
		/clone="NT2RM4001663"								
		/clone_id="NT2RM4"								
		/cell_type="teratocarcinoma"								
		/cell_line="NT2"								
		/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal								
		precursor cells"								
		150 a	227 c	229 g	137 t	3 others				
		Query Match	50.6%	Score 83;	DB 9;	Length 746;				
		Best Local Similarity	69.3%	Pred. No. 1.8e-14;						
		Matches 113; Conservative	0;	Mismatches 50;	Indels 0;	Gaps 0;				
2	CACCGGCAATCAAGCAAGCA	AAATATTTTGTCTATGTGAAGATGAGAACATGATGACATC	61							
78	CACCGTGTATCTCAAGTCA	CAACACATTTTGTCTGCGACGCCATTGAGATGAGACACATG	137							
62	TGCATATAAATCTTGAGAT	TACAGATTTTGGTGGCGGAGGAATGGACACAGACACACC	121							
138	GAGCACAAGACCTCGAAT	CATCAGCATTTTGGCTGGCGGCGGAGATGGCACAAAAACACA	197							
122	AAATGAGCAGACGACGAC	CCTATGCTGATGGCCCCAGAG	164							
198	CAATGAGTGTCCGCGGCG	CACCTACGCTGATGGCTCTGAGG	240							
RESULT 10	LOCUS	DEFINITION	AGENCOURT_8234446	lupski_symptathetic_trunk	Homo sapiens cDNA clone	873 bp	mRNA	linear	EST 16-JUL-2002	

IMAGE:618692 5', mRNA sequence.
ACCESSION BQ719600
VERSION BQ719600.1 GI:21858497
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 873)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13584 row: 1 column: 05
High quality sequence stop: 620.

FEATURES
source
1. 873
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:618692"
/clone_lib="Lupski_sympathetic_trunk"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/note="Vector: PCWY-SPORT6 (Life Technologies); Site:1:
NotI; Site:2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGCCG-3' and
5'-GACTAGTCTAGATCGGAGCGGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

BASE COUNT 167 a 271 c 270 g 165 t
ORIGIN

Query Match 50.6%; Score 83; DB 14; Length 873;
Best Local Similarity 69.3%; Pred. No. 1.9e-14;
Matches 113; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 2 CACCGGACATCAAGGAGGAATATTTGCTCTGAGAAATGACATGATGATC 61
DB 376 CACCGGATCTCAAGTCCAAACAAATTTGCTCTGAGCCCATGAGATGACGATG 435
QY 62 TGCATATAAACTTTGAAGATTACAGATTTTGGTGGCGAGGAAATGACAGACAC 121
DB 436 GACGACAAAGCCCTGAAGATCACGCACTTGGCTGGCCCGAAGTGGCAAAACACA 435
QY 122 AAATATGACACAGGACACCTATGCTTGATGGCCCGACAG 164
DB 496 CAATATGATGCCGCGGACCTACGCTGATGATGCTGTGAG 538

RESULT 11
LOCUS BQ227232 895 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT_7567317 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6060488
5', mRNA sequence.
ACCESSION BQ227232
VERSION BQ227232.1 GI:20408632
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 895)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DFP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13328 row: n column: 09
High quality sequence stop: 673.

FEATURES
source
1. 895
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6060488"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: PCWY-SPORT6; Site:1: NotI;
Site:2: SalI; cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

BASE COUNT 176 a 281 c 276 g 160 t 2 others
ORIGIN

Query Match 50.6%; Score 83; DB 14; Length 895;
Best Local Similarity 69.3%; Pred. No. 2e-14;
Matches 113; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 2 CACCGGACATCAAGGAGGAATATTTGCTCTGAGAAATGACATGATGATC 61
DB 242 CACCGGATCTCAAGTCCAAACAAATTTGCTCTGAGCCCATGAGATGACGATG 301
QY 62 TGCATATAAACTTTGAAGATTACAGATTTTGGTGGCGAGGAAATGACAGACAC 121
DB 302 GACGACAAAGCCCTGAAGATCACGCACTTGGCTGGCCCGAAGTGGCAAAACACA 361
QY 122 AAATATGACACAGGACACCTATGCTTGATGGCCCGACAG 164
DB 362 CAATATGATGCCGCGGACCTACGCTGATGATGCTGTGAG 404

RESULT 12
LOCUS BM549532 1057 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6554238 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548665
5', mRNA sequence.
ACCESSION BM549532
VERSION BM549532.1 GI:18785023
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1057)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: AFCC/DCTD/DFP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM12257 row: p column: 10
High quality sequence stop: 614.

FEATURES
source
Location/Qualifiers

1.1057
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5548665"
/clone_1lb="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: PCMV-SPORE6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by life
Technologies."

BASE COUNT 201 a 319 c 355 g 179 t 3 others
ORIGIN

Query Match 50.6%; Score 83; DB 13; Length 1057;
Best Local Similarity 69.3%; Pred. No. 2.1e-14;

Matches 113; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 2 CACCGGACATCAAGCAGGAAATATTTGCTCTGAGAGATGACATG 61
||||| || ||||| || ||||| || ||||| || |||||

Db 371 CACCGTATCTCAAGTCCAAACAACTTTTGTCTGTCAGCCCATTTGAGCATG 430
| || || ||||| || ||||| ||||| || ||||| ||||| |||||

QY 62 TGCATTAACCTTGAAGATTACAGATTTGGTGGCGAGGAATGGCAGCAGCACC 121
| || || ||||| || ||||| ||||| || ||||| ||||| |||||

Db 431 GAGCACAAGACCTGAGAGATCACCGACTTTGGCTGGCCCGAAGATGGCACAACACCA 490
| || || ||||| || ||||| ||||| || ||||| ||||| |||||

QY 122 AAATGACACAGCAGGACCTATGCTGTGATGGCCCGACAGAG 164
||||| || ||||| || ||||| ||||| || |||||

Db 491 CAATGATGTCGGCGGCACCTAGCCTGATGGCTCTGAGG 533
||||| || ||||| || ||||| ||||| || |||||

RESULT 13

LOCUS BQ709288 1278 bp mRNA linear EST 16-JUL-2002

DEFINITION AGENCOURT_7975607 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:5215047

ACCESSION BQ709288

VERSION BQ709288.1 GI:21848187

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2383 row: f column: 08

High quality sequence stop: 367.

Location/Qualifiers

1.1278

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6215047"

/clone_1lb="NIH_MGC_113"

/lab_host="DH10B (phage-resistant)"

/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; CDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGCAG(G). Library constructed by Ling Hong in the

Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT 280 a 375 c 419 g 200 t 4 others
ORIGIN

Query Match 47.9%; Score 78.6; DB 14; Length 1278;

Best Local Similarity 68.8%; Pred. No. 4.7e-13;

Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 8 GACATCAAGCAGGAATATTTGCTACTTGAAGATGAGATGACATCTGCAAT 67
|| ||||| || ||||| || || || || || |||||

Db 2 GATCTCAAGTCCAAACAACTTTTGTCTGCTGAGCCATTGAGAGTACGACATGAGCAGC 61
| || || ||||| || ||||| ||||| || ||||| ||||| |||||

QY 68 AAAACTTTGAAGATTACAGATTTGGGTGGCGAGGAATGGCAGCAGCAATG 127
|| || ||||| || || ||||| ||||| || ||||| ||||| |||||

Db 62 AAGACCTGAAGATCACCGACTTTGGCTGGCCGAGAGTGGCAGCAACACACCAATG 121
| || || ||||| || || ||||| ||||| || ||||| ||||| |||||

QY 128 AGCAGCAGCAGCAGCCTATGCTGATGGCCCGAGAG 164
|| || || ||||| || ||||| ||||| || |||||

Db 122 AGTGGCGGCGGACCTAGCCTGATGGCTCTGAGG 158
||||| || ||||| || ||||| ||||| || |||||

RESULT 14 BQ751808 863 bp mRNA linear EST 15-MAY-2001

LOCUS 6027307451 NIH_MGC_43 Homo sapiens CDNA clone IMAGE:4874228 5',

DEFINITION mRNA sequence.

ACCESSION BQ751808

VERSION BQ751808.1 GI:14062461

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1753 row: j column: 11

High quality sequence stop: 856.

Location/Qualifiers

1.863

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4874218"

/clone_1lb="NIH_MGC_43"

/tissue_type="normal pigmented retinal epithelium"

/lab_host="DH10B (phage-resistant)"

/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; CDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCAGCAG(G). Library constructed by Ling Hong

in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library. "

BASE COUNT 167 a 276 c 280 g 140 t

ORIGIN

Query Match 45.9%; Score 75.2; DB 12; Length 863;

Best Local Similarity 70.1%; Pred. No. 4.4e-12;

Matches 101; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY	21	GAAATATTTTGGCTACTTGAGAAAGATAGAACATGATGCATTAATAAATTGGAAGA	80
Dd	1	GCACAATTTTGGCTGCTGCGACGCCCATTTGAGAGTGCAGCAATGGACGACAAGACCTCTGAAGA	60
QY	81	TTCAGATTTTGGGTGGGCGCAGGAGTAATGSCAAGACCACCAAATTTGACACAGCAGGCA	140
Dd	61	TCACCGACTTTTGCCCTTGGCCCCGAGAGTAGTGGCACAAAACACACAATTTGAGTGGCGCGGSCA	120
QY	141	CCTATGCTGGATGGGCCCCAGAG	164
Dd	121	CCTAGCCTGGATGGCTCCTGAGG	144

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OY      122  AAAATGACACACAGGAGGACCTTATGCTGTATGGCCCCCAAG 164
          | | | | | | | | | | | | | | | | | | | | | |
Db      414  CAGATGATGCTGTGGGGCAGCTACGCTTGATGGCTCCGAGG 456

Search completed: December 13, 2002, 23:27:10
Job time : 2161 secs

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RESULT	15
BQ266193	
LOCUS	
DEFINITION	BQ266193 461 bp mRNA "linear EST 07-MAY-2002 MUSC_fflie05.y1 NCL_CGAP_Mamts Mus musculus cDNA IMAGE:286512
ACCESION	MJSC_fflie05.y1 NCL_CGAP sequence.
VERSION	BQ266193
KEYWORDS	BQ266193..1 GI:20491258
SOURCE	EST.
ORGANISM	house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
TITLE	Unpublished (1997)
JOURNAL	Contact: Robert Strausberg, Ph.D.
COMMENT	

Tissue Procurement: Lothar Hennighausen/Robin Humphreys
 cDNA Library Preparation: Life Technologies
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
 MGI:1046284
 Plate: LLAW7069 row: J column: 9
 Seq primer: M13RPI reverse primer (ABI).
 Location/Qualifiers
 1. .461

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BASE COUNT      94 a      137 c      135 g      95 t
ORIGIN
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:2665512"
/clone_id="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCW-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennigausen/Robin Humphreys,
Nir"

```

	Query Match	45.7%	Score 75;	DB 14;	Length 461;
	Best Local Similarity	66.38;	Pred. No. 4.1e-12;		
	Matches 108; Conservative	0;	Mismatches 55;	Indels 0;	Gaps 0;
QY	2	CACGGGACATCAAGCGCAGAATAATTTCGTACTTGAAGATAGAAACATGATGACATC	61		
Dd	294	CACCGAACAACCTGAAGTCCAACACACATTTCTGTGCTGCAGGCCCATCGAGGGGACGACATG	353		
QY	62	TGCATTAATAACTTGAAGATTACAGATTTTGATTTGGCTGGCGAGGGAATGACACGAGCACACC	121		
Dd	354	GAACACAGAGCCCTTAAGAGATTACGACTTGGCCCTCGCCCCGAGAGTGCCACAAAACACACC	413		

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OY      122  AAAATGACACACAGGAGGACCTTATGCTGTATGGCCCCCAAG 164
          | | | | | | | | | | | | | | | | | | | | | |
Db      414  CAGATGATGCTGTGGGGCAGCTACGCTTGATGGCTCCGAGG 456

Search completed: December 13, 2002, 23:27:10
Job time : 2161 secs

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Search completed: December 13, 2002, 23:27:10
Job time : 2181 secs